

SEQUENCE LISTING

<110> Christopher T. Ritchlin
Sally Haas-Smith
Edward Schwarz

<120> Methods and Compositions Related to
Joint Inflammation Diseases

<130> 21108.0031U2

<140> Unassigned

<151> 2003-03-12

<150> 60/454,573

<151> 2003-03-14

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 1

ctatttcaga gcgcatatgg at

22

<210> 2

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 2

tatgagaact tgggattttg atgc

24

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 3

ttaagccagt gcttcacggg

20

<210> 4

<211> 22

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 4
 acgtagacca cgatgatgtc gc 22

<210> 5
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 5
 gctaacctca ccttcgag 18

<210> 6
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 6
 tgattggacc tggttacc 18

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 7
 gctctccaga acatcatccc tgcc 24

<210> 8
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 8
 cgttgtcata ccaggaaatg agctt 25

<210> 9
 <211> 2225
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 9

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cggggagcca ctgccaggac ctctgtgaac cggtcggggc gggggccgcc tggccgggag 60
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ctccggggcgc cgcgccatgc gccggggccag ccgagactac ggcaagtacc tgcgcagctc 180
ggaggagatg ggcagcggcc ccggcgctccc acacgagggg ccgctgcacc ccgcgccttc 240
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gctgggactg ggccaggagg tctgcagcat cgctctgttc ctgtactttc gagcgagat 360
ggatcctaac agaatacag aagacagcac tcaactgttt tatagaatcc tgagactcca 420
tgaaaacgca gatttgcagg actcgactct ggagagtga gacacactac ctgactcctg 480
caggaggatg aaacaagcct ttcagggggc cgtgcagaag gaactgcaac acattgtggg 540
gccacagcgc ttctcaggag ctccagctat gatggaaggc tcatggttgg atgtggcca 600
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gggggtcaca gtctctgggt ctaaccctg gacatgtgcc actgagaacc ttgaaattaa 1440
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tactgaaatc tgtcaggagt atttatgcaa ttattgaaca ggtgtctttt tttacaagag 2040
ctacaaattg taaattttgt ttctttttt tcccatagaa aatgtactat agtttatcag 2100
ccaaaaaaca atccactttt taatttagtg aaagttattt tattatactg tacaataaaa 2160
gcattgtctc tgaatgttaa ttttttggtg caaaaaataa atttgtacga aaacctgaaa 2220
aaaaa 2225

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<210> 10

<211> 316

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 10

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Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
1           5           10          15
Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
20           25           30

```

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80
 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95
 Asn Ala Asp Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110
 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125
 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140
 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160
 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175
 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190
 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205
 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220
 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240
 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255
 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 290 295 300
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 305 310 315

<210> 11

<211> 2201

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 11

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ggccaaagcc gggctccaag tcggcgcccc acgtcgaggc tccgccgcag cctccggagt 60
tggccgcaga caagaagggg agggagcggg agagggagga gagctccgaa gcgagagggc 120
cgagcgccat gcgccgcgcc agcagagact acaccaagta cctgcgtggc tcggaggaga 180
tgggcgggcg ccccgagacc ccgcacgagg gccccctgca cgccccgccg ccgcctgcgc 240
cgcaccagcc ccccgccgcc tcccgtcca tggtcgtggc cctcctgggg ctggggctgg 300
gccaggttgt ctgcagcgtc gccctgttct tctatttcag agcgcagatg gatacctaata 360
gaatatcaga agatggcact cactgcattt atagaatttt gagactccat gaaaatgcag 420
attttcaaga cacaactctg gagagtcaag atacaaaatt aatacctgat tcatgtagga 480
gaattaaaca ggcctttcaa ggagctgtgc aaaaggaatt acaacatata gttggatcac 540
agcacatcag agcagagaaa gcatggttgg atgggtcatg gttagatctg gccaagagga 600
gcaagcttga agctcagcct tttgctcatt tcaactattaa tgccaccgac atcccatctg 660
gttcccataa agtgagtctg tcctcttggg accatgatcg gggttgggcc aagatctcca 720
acatgacttt tagcaatgga aaactaatag ttaatcagga tggcttttat tacctgtatg 780

```

```

ccaacatttg ctttcgacat catgaaactt caggagacct agctacagag tatcttcaac 840
taatggtgta cgtcactaaa accagcatca aaatcccaag ttctcatacc ctgatgaaag 900
gaggaagcac caagtattgg tcagggaatt ctgaattcca tttttattcc ataaacggtg 960
gtggattttt taagttacgg tctggagagg aaatcagcat cgaggctctcc aacctctcct 1020
tactggatcc ggatcaggat gcaacatact ttggggcctt taaagtctga gatatagatt 1080
gagccccagt ttttgagtg ttatgtattt cctggatgtt tggaaacatt ttttaaaaca 1140
agccaagaaa gatgtatata ggtgtgtgag actactaaga ggcattggccc caacggtaca 1200
cgactcagta tccatgctct tgaccttgta gagaacacgc gtatttacct gccagtggga 1260
gatgttagac tcatggtgtg ttacacaatg gtttttaaat tttgtaatga attcctagaa 1320
ttaaaccaga ttggagcaat tacgggttga ccttatgaga aactgcatgt gggctatggg 1380
aggggttggg ccctgggtcat gtgccccttc gcagctgaag tggagagggt gtcacttagc 1440
gcaattgaag gatcatctga aggggcaaat tcttttgaat tgttacatca tgctggaacc 1500
tgcaaaaaat actttttcta atgaggagag aaaatatatg tatttttata taatatctaa 1560
agttatattt cagatgtaat gttttctttg caaagtattg taaattatat ttgtgctata 1620
gtatttgatt caaaatattt aaaaatgtct tgctgttgac atatttaatg ttttaaattg 1680
acagacatat ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag 1740
gggaaaaaaa tgttggttcc taatatcaaa tgcagtatat ttcttcgttc tttttaagtt 1800
aatagatttt ttcagacttg tcaagcctgt gcaaaaaaat taaaatggat gccttgaata 1860
ataagcagga tgttgggcac caggtgcctt tcaaatttag aaactaattg actttagaaa 1920
gctgacattg ccaaaaagga tacataatgg gccactgaaa tttgtcaaga gtagtatat 1980
aattgttgaa caggtgtttt tccacaagtg ccgcaaattg tacctttttt ttttttcaa 2040
aatagaaaag ttattagtgg tttatcagca aaaaagtcca attttaattt agtaaatggt 2100
attttatact gtacaataaa aacattgcct ttgaatgtta attttttggg acaaaaataa 2160
atztatatga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2201

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<210> 12

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 12

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Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
 1           5           10          15
Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
 20          25          30
Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 35          40          45
Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 50          55          60
Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65          70          75          80
Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 85          90          95
Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
100         105         110
Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
115         120         125
Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
130         135         140
Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
145         150         155         160
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
165         170         175
Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
180         185         190
Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195         200         205

```

Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His
210						215					220				
His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val
225					230					235					240
Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met
				245					250					255	
Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe
			260					265					270		
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu
	275					280						285			
Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp
	290					295					300				
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp			
305					310					315					

<210> 13

<211> 3136

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 13

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ccgctgaggc cgcgggcgccc gccagcctgt cccgcgccat ggccccgcgc gcccggcggc 60
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tgcagatcgc tccctccatgt accagtgaga agcattatga gcatctggga cgggtgctgta 180
acaaatgtga accagaaaag tacatgtctt ctaaactgcac tactacctct gacagtgtat 240
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tgcataaagt ttgtgataca ggcaaggccc tgggtggccgt ggtcgccggc aacagcacga 360
ccccccggcg ctgcgcgtgc acggctgggt accactggag ccaggactgc gagtgtgtcc 420
gccgcaacac cgagtgcgcg cggggcctgg gcgcccagca cccgttgtag ctcaacaagg 480
acacagtgtg caaaccttgc cttgcaggct acttctctga tgccttttcc tccacggaca 540
aatgcagacc ctggaccaac tgtaccttcc ttggaaagag agtagaacat catgggacag 600
agaaatccga tgcggtttgc agttcttctc tgccagctag aaaaccacca aatgaacccc 660
atgtttactt gcccgtttta ataattctgc ttctcttcgc gtctgtggcc ctgggtggctg 720
ccatcatctt tggcgtttgc tataggaaaa aagggaagac actcacagct aatttgtggc 780
actggatcaa tgaggcttgt ggccgcctaa gtggagataa ggagtcctca ggtgacagtt 840
gtgtcagtac acacacggca aactttggtc agcaggagag atgtgaaggt gtcttactgc 900
tgactctgga ggagaagaca tttccagaag atatgtgcta cccagatcaa ggtggtgtct 960
gtcagggcac gtgtgtagga ggtggtccct acgcacaagg cgaagatgcc aggatgtctt 1020
cattggtcag caagaccgag atagaggaag acagcttcag acagatgccc acagaagatg 1080
aatacatgga caggccctcc cagcccacag accagttact gttcctcact gagcctggaa 1140
gcaaatccac acctccttcc tctgaacccc tggaggtggg ggagaatgac agtttaagcc 1200
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tcccggaccc gtgcggcgcc cccgaggggc tgcgggagcc ggagaaggcc tcgagggccg 1860
tgcaggagca aggcggggcc aaggcttgag cgcggcccat ggctgggagc ccgaagctcg 1920
gagccagggc tcgcgagggc agcaccgcag cctctgcccc agccccggcc acccagggat 1980
cgatcggtac agtcgaggaa gaccacccgg cattctctgc ccactttgcc ttccaggaaa 2040
tgggcttttc aggaagtga ttgatgagga ctgtcccat gccacggat gctcagcagc 2100

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ccgccgcact ggggcagatg tctcccctgc cactcctcaa actcgcagca gtaattttgtg 2160
gcactatgac agctattttt atgactatcc tgttctgtgg ggggggggtc tatgttttcc 2220
ccccatattt gtattccttt tcataacttt tcttgatata tttcctccct cttttttaat 2280
gtaaagggtt tctcaaaaat tctcctaaag gtgagggtct ctttcttttc tcttttccct 2340
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aaatttttaa aaaaaa 3136

```

<210> 14

<211> 616

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 14

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Met Ala Pro Arg Ala Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu
1          5          10          15
Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro
20          25          30
Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
35          40          45
Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
50          55          60
Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
65          70          75          80
Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
85          90          95
Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
100          105          110
Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
115          120          125
Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
130          135          140
Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
145          150          155          160
Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
165          170          175
Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
180          185          190
Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
195          200          205
Val Tyr Leu Pro Gly Leu Ile Leu Leu Leu Phe Ala Ser Val Ala
210          215          220
Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
225          230          235          240
Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
245          250          255

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Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
      260      265      270
Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
      275      280      285
Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
      290      295      300
Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln
305      310      315      320
Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
      325      330      335
Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
      340      345      350
Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
      355      360      365
Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
      370      375      380
Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
385      390      395      400
Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
      405      410      415
Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
      420      425      430
His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
      435      440      445
Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro
      450      455      460
Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro
465      470      475      480
Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly
      485      490      495
Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly
      500      505      510
Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn
      515      520      525
Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly
      530      535      540
Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala
545      550      555      560
Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala
      565      570      575
Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys
      580      585      590
Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val
      595      600      605
Gln Glu Gln Gly Gly Ala Lys Ala
      610      615

```

<210> 15

<211> 2116

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 15

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cgcccagccc gcccgaccg cgccatggcc ccgcgcgccc ggcggcgccg ccagctgccc 60
gcgccgctgc tggcgctctg cgtgctgctc gttccactgc aggtgactct ccaggtcact 120
cctccatgca cccaggagag gcattatgag catctcggac ggtgttcgag cagatgcgaa 180

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ccaggaaagt acctgtcctc taagtgcact cctacctccg acagtgtgtg tctgccctgt 240
ggccccgatg agtacttgga cacctggaat gaagaagata aatgcttgct gcataaagtc 300
tgtgatgcag gcaaggccct ggtggcggtg gatcctggca accacacggc cccgcgtcgc 360
tgtgcttgca cggctggcta ccactggaac tcagactgcg agtgctgccg caggaacacg 420
gagtgtgcac ctggcttcgg agctcagcat cccttgacgc tcaacaagga tacgggtgtgc 480
acaccctgcc tcctgggctt cttctcagat gtcttttcgt ccacagacaa atgcaaacct 540
tggaccaact gcaccctcct tggaaagcta gaagcacacc aggggacaac ggaatcagat 600
gtgggtctgca gctcttccat gacactgagg agaccaccca aggaggccca ggcttacctg 660
cccagttctca tcgttctgct cctcttcata tctgtggtag tagtggctgc catcatcttc 720
ggcgtttact acaggaaggg agggaaagcg ctgacagcta atttgtggaa ttgggtcaat 780
gatgcttgca gtagtctaag tggaaataag gagtccctcag gggaccgttg tgctgggtcc 840
cactcggcaa cctccagtc gcaagaagtg tgtgaaggta tcttactaat gactcgggag 900
gagaagatgg ttccagaaga cgggtgctga gtctgtgggc ctgtgtgtgc ggcaggtggg 960
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gtggattctg agggctgtga cttcactgag cctccgagca gaactgactc tatgcccggtg 1260
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gagaggggag cctcagggtc cgggagctcc cccagtgacc agccacctgc ctctgggaac 1560
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gagtcggagc ccgtgggccg ccctgtgcag gaggagacgc tggcacacag agactccttt 1740
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ggggcacccc ggcagaagga cgggacatcg cggccggtgc aggagcaggg tggggcgagc 1860
acttcactcc ataccaggg gtccggacaa tgtgcagaat gacctcacct tctctgtctg 1920
ccctgggtgc agggcaccag tgcctttcca aaaacatggt gtagctagcc actgtgcacc 1980
tccctactgg tgcaggctgc tggcatgggt atggagccca cctctcactt cctccagtgc 2040
ccctctcctc tgcctcctac cacctggcat cattcagttt ggctttttt tgcaacgttg 2100
gtgtcctgca ttattg 2116

```

<210> 16

<211> 625

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 16

```

Met Ala Pro Arg Ala Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu
 1           5           10           15
Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr
          20           25           30
Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
          35           40           45
Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
          50           55           60
Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
          65           70           75           80
Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
          85           90           95
Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
          100          105          110
Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys
          115          120          125

```

Arg	Arg	Asn	Thr	Glu	Cys	Ala	Pro	Gly	Phe	Gly	Ala	Gln	His	Pro	Leu
130						135					140				
Gln	Leu	Asn	Lys	Asp	Thr	Val	Cys	Thr	Pro	Cys	Leu	Leu	Gly	Phe	Phe
145					150					155					160
Ser	Asp	Val	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Lys	Pro	Trp	Thr	Asn	Cys
				165					170					175	
Thr	Leu	Leu	Gly	Lys	Leu	Glu	Ala	His	Gln	Gly	Thr	Thr	Glu	Ser	Asp
			180					185					190		
Val	Val	Cys	Ser	Ser	Ser	Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala
		195					200					205			
Gln	Ala	Tyr	Leu	Pro	Ser	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val
	210					215					220				
Val	Val	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly
225					230					235					240
Lys	Ala	Leu	Thr	Ala	Asn	Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser
				245					250					255	
Ser	Leu	Ser	Gly	Asn	Lys	Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser
			260					265					270		
His	Ser	Ala	Thr	Ser	Ser	Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu
	275					280						285			
Met	Thr	Arg	Glu	Glu	Lys	Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys
	290					295					300				
Gly	Pro	Val	Cys	Ala	Ala	Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser
305					310					315					320
Arg	Thr	Phe	Thr	Leu	Val	Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser
				325					330					335	
Arg	Lys	Ile	Pro	Thr	Glu	Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Ser	Gln	Pro
			340					345					350		
Ser	Thr	Gly	Ser	Leu	Leu	Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro
		355					360					365			
Pro	Phe	Gln	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln
	370					375					380				
Cys	Phe	Thr	Gly	Thr	Glu	Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe
385					390					395					400
Thr	Glu	Pro	Pro	Ser	Arg	Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys
				405					410					415	
His	Leu	Thr	Lys	Glu	Ile	Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val
			420					425					430		
Ser	Ser	Asn	Ser	Thr	Asp	Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly
		435				440						445			
Glu	Asp	His	Glu	Pro	Phe	Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro
	450					455					460				
Gln	Cys	Ala	Tyr	Ser	Met	Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met
465					470					475					480
Ala	Glu	Ala	Gly	Val	Arg	Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala
				485					490					495	
Ser	Gly	Ser	Gly	Ser	Ser	Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn
			500					505					510		
Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met
		515					520					525			
Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln
	530					535					540				
Glu	Gly	Pro	Gly	Ser	Ala	Glu	Pro	Glu	Ser	Glu	Pro	Val	Gly	Arg	Pro
545					550					555					560
Val	Gln	Glu	Glu	Thr	Leu	Ala	His	Arg	Asp	Ser	Phe	Ala	Gly	Thr	Ala
				565					570					575	
Pro	Arg	Phe	Pro	Asp	Val	Cys	Ala	Thr	Gly	Ala	Gly	Leu	Gln	Glu	Gln
			580					585					590		
Gly	Ala	Pro	Arg	Gln	Lys	Asp	Gly	Thr	Ser	Arg	Pro	Val	Gln	Glu	Gln
		595					600					605			

Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala
 610 615 620
 Glu
 625

<210> 17
 <211> 1669
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 17
 ctccctcagc aaggacagca gaggaccagc taagagggag agaagcaact acagaccccc 60
 cctgaaaaca accctcagac gccacatccc ctgacaagct gccaggcagg ttctcttcct 120
 ctcacatact gaccacaggc tccacctct ctcccctgga aaggacacca tgagcactga 180
 aagcatgatc cgggacgtgg agctggccga ggaggcgctc cccaagaaga cagggggggc 240
 ccagggctcc aggcggtgct tgttcctcag cctcttctcc ttcctgatcg tggcaggcgc 300
 caccacgctc ttctgcctgc tgcactttgg agtgatcggc cccagagggg aagagttccc 360
 cagggacctc tctctaata gcccctctgg ccaggcagtc agatcatctt ctccaacccc 420
 gagtgacaag cctgtagccc atgttgtagc aaacctcaa gctgaggggc agctccagt 480
 gctgaaccgc cgggccaatg cctcctctgg caatggcgctg gagctgagag ataaccagct 540
 ggtggtgcca tcagagggcc tgtacctcat ctactcccag gtcctcttca agggccaagg 600
 ctgcccctcc acccatgtgc tcctcaccca caccatcagc cgcacgcgcg tctcctacca 660
 gaccaaggtc aacctcctct ctgccatcaa gagcccctgc cagagggaga cccagagggg 720
 ggctgaggcc aagccctggt atgagcccat ctatctggga ggggtcttcc agctggagaa 780
 gggtgaccga ctcagcgctg agatcaatcg gcccgactat ctcgactttg ccgagtctgg 840
 gcagggtctac tttgggatca ttgccctgtg aggaggacga acatccaacc ttcccaaacg 900
 cctcccctgc cccaatccct ttattacccc ctccctcaga caccctcaac ctcttctggc 960
 tcaaaaagag aattgggggc ttagggtcgg aacccaagct tagaacttta agcaacaaga 1020
 ccaccacttc gaaacctggg attcaggaat gtgtggcctg cacagtgaag tgctggcaac 1080
 cactaagaat tcaaaactgg gcctccagaa ctcactgggg cctacagctt tgatccctga 1140
 catctggaat ctggagacca gggagccttt gggttctggc agaatgctgc aggacttgag 1200
 aagacctcac ctagaaattg acacaagtgg accttaggcc ttcctctctc cagatgtttc 1260
 cagacttctt tgagacacgg agcccagccc tcgccatgga gccagctccc tctatttatg 1320
 tttgcacttg tgattattta ttatttattt attatttatt tatttacaga tgaatgtatt 1380
 tatttggggag accgggggat cctgggggac ccaatgtagg agctgccttg gctcagacat 1440
 gttttccgtg aaaacggagc tgaacaatag gctgttccca tgtagcccc tggcctctgt 1500
 gccttctttt gattatgttt tttaaaatat ttatctgatt aagttgtcta aacaatgctg 1560
 atttggtgac caactgtcac tcattgctga gcctctgctc cccaggggag ttgtgtctgt 1620
 aatcgcccta ctattcagtg gcgagaaata aagtttgctt agaaaagaa 1669

<210> 18
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 18
 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1 5 10 15
 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

```

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
   35           40           45
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
   50           55           60
Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
   65           70           75           80
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
           85           90           95
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
           100          105          110
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
           115          120          125
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
           130          135          140
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
           145          150          155          160
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
           165          170          175
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
           180          185          190
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
           195          200          205
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
           210          215          220
Gln Val Tyr Phe Gly Ile Ile Ala Leu
           225          230

```

<210> 19

<211> 1619

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 19

```

cctcagcgag gacagcaagg gactagccag gagggagaac agaaactcca gaacatcttg 60
gaaatagctc ccagaaaagc aagcagccaa ccaggcaggt tctgtccctt tactcactg 120
gccaagggcg ccacatctcc ctccagaaaa gacaccatga gcacagaaag catgatccgc 180
gacgtggaac tggcagaaga ggcactcccc caaaagatgg ggggcttcca gaactccagg 240
cgggtgcctat gtctcagcct cttctcattc ctgcttggtg caggggccac cacgctcttc 300
tgtctactga acttcggggg gatcgggtccc caaagggatg agaagttccc aaatggcctc 360
cctctcatca gttctatggc ccagaccctc acactcagat catcttctca aaattcgagt 420
gacaagcctg tagcccacgt cgtagcaaac caccaagtgg aggagcagct ggagtggctg 480
agccagcgcg ccaacgcctt cctggccaac ggcattggatc tcaaagacaa ccaactagt 540
gtgccagccg atgggttgta cctgtgttac tcccagggtc tcttcaaggg acaaggctgc 600
cccgactacg tgctcctcac ccacaccgtc agccgatttg ctatctcata ccaggagaaa 660
gtcaacctcc tctctgccgt caagagcccc tgccccaagg acaccctga gggggctgag 720
ctcaaaccct ggtatgagcc catatacctg ggaggagtct tccagctgga gaagggggac 780
caactcagcg ctgaggtcaa tctgccaag tacttagact ttgcggagtc cgggcaggtc 840
tactttggag tcattgctct gtgaagggaa tgggtgttca tccattctct acccagcccc 900
cactctgacc ctttactct gacccttta ttgtctactc ctcagagccc ccagtctgtg 960
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acaactactc agaaacacaa gatgctggga cagtgcctg gactgtgggc ctctcatgca 1080
ccaccatcaa ggactcaaat gggctttccg aattcactgg agcctcgaat gtccattcct 1140
gagttctgca aaggagaggt ggtcagggtt cctctgtctc agaatgaggc tggataagat 1200
ctcaggcctt cctaccttca gacctttcca gactcttccc tgaggtgcaa tgcacagcct 1260
tcctcacaga gccagcccc ctctatttat atttgactt attatttatt atttatttat 1320
tatttattta tttgcttatg aatgtattta tttggaaggc cgggggtgtc tggaggaccc 1380

```

```

agtgtgggaa gctgtcttca gacagacatg ttttctgtga aaacggagct gagctgtccc 1440
cacctggcct ctctaccttg ttgcctcctc ttttgcttat gtttaaaaca aaatatttat 1500
ctaacccaat tgtcttaata acgctgattt ggtgaccagg ctgtcgctac atcactgaac 1560
ctctgtctccc cacgggagcc gtgactgtaa ttgccctaca gtcaattgag agaaataaa 1619

```

<210> 20
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

```

<400> 20
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1          5          10          15
Leu Pro Gln Lys Met Gly Gly Phe Gln Asn Ser Arg Arg Cys Leu Cys
          20          25          30
Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
          35          40          45
Cys Leu Leu Asn Phe Gly Val Ile Gly Pro Gln Arg Asp Glu Lys Phe
          50          55          60
Pro Asn Gly Leu Pro Leu Ile Ser Ser Met Ala Gln Thr Leu Thr Leu
          65          70          75          80
Arg Ser Ser Ser Gln Asn Ser Ser Asp Lys Pro Val Ala His Val Val
          85          90          95
Ala Asn His Gln Val Glu Glu Gln Leu Glu Trp Leu Ser Gln Arg Ala
          100          105          110
Asn Ala Leu Leu Ala Asn Gly Met Asp Leu Lys Asp Asn Gln Leu Val
          115          120          125
Val Pro Ala Asp Gly Leu Tyr Leu Val Tyr Ser Gln Val Leu Phe Lys
          130          135          140
Gly Gln Gly Cys Pro Asp Tyr Val Leu Leu Thr His Thr Val Ser Arg
          145          150          155          160
Phe Ala Ile Ser Tyr Gln Glu Lys Val Asn Leu Leu Ser Ala Val Lys
          165          170          175
Ser Pro Cys Pro Lys Asp Thr Pro Glu Gly Ala Glu Leu Lys Pro Trp
          180          185          190
Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
          195          200          205
Gln Leu Ser Ala Glu Val Asn Leu Pro Lys Tyr Leu Asp Phe Ala Glu
          210          215          220
Ser Gly Gln Val Tyr Phe Gly Val Ile Ala Leu
          225          230          235

```

<210> 21
 <211> 2254
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

```

<400> 21
ccaacaatct gtgtggttgt ttttctgtgt tcctccaatg gtagggcctc tgttcaccag 60
tgccgtctct tcttttagct gtaagaaaag cctggagtgc acgaagttgt gcctacccca 120
gattgagaat gtttaaggga ctgaggactc aggtgaggag aggtgacctg gtgccccatgc 180
tcacctgccc tctccctctt cttgccccca cccgtccatc catccaccc atccatctat 240

```

```

ccttgcgcc cccctctgcc cgctcctctg accaacacct gctttgtctg caggcaccac 300
agtgtgttg cccctggtca ttttcttttg tctttgcctt ttatccctcc tcttcattgg 360
tttaatgtat cgctaccaac ggtggaagtc caagctctac tccattggtg agtgggggct 420
ttgggagggg gagggagctg gtgggggtga gggaggacat ggggtgggtgc gatggacatg 480
tgtggagggg ggtgaggagt gtccctcag ttcataccgc tggggactct gggcagaagg 540
tggccctgga tggctgggga gatgtcgagc tgcatacagta gctctctcgt ccctggggcc 600
acataggccc tgaggcatgt caccacaagt cccactgcc agctgagtcc agggtgccag 660
ggctgagaga ggaagtgaag tttatgatgc tttctttctt tttcctcagt ttgtgggaaa 720
tcgacacctg aaaaagaggt gagatgaaat gagagagtta ctcccaaagt tccctgacca 780
ttccttataa ttgcctaagt ctcagatccc ctggaatcat ccttcacttt ccggggggctc 840
gcctcattcc ctctaagtcc caacccccac gtagaataaa gagggccggg gctggttttc 900
gctgcgcac taatctgcgc caccttctct ctttcagggg gagcttgaag gaactactac 960
taagcccctg gcccacaaacc caagcttcag tccactcca ggcttcaccc ccaccctggg 1020
cttcagtcctc gtgcccagtt ccaccttcac ctccagctcc acctataccc ccggtgactg 1080
tcccaacttt gcggctcccc gcagagaggt ggcaccaccc tatcaggggg ctgaccccat 1140
ccttgcgaca gccctcgct cggaccccat ccccaacccc cttcagaagt gggaggacag 1200
cgcccacaag ccacagagcc tagacagtgc gtttctcccg cggctggaga cgaggaggct 1260
gggggagggc cgggggagcg cgggagcggt cagagggggac cacgagaggc ggagggcgcg 1320
ggatgcgggg cggggcctgg ggttgccgcc cgagggctcac cggcccgcgt ccccgagct 1380
gatgaccccc cgacgctgta cgccgtgggt gagaacgtgc ccccggttgc ctggaaggaa 1440
ttcgtgcggc gcctagggt gagcgaccac gagatcgatc ggctggagct gcagaacggg 1500
cgctgcctgc gcgagcgca atacagcatg ctggcgacct ggagggcgcg cacgcccgcg 1560
cgcgaggcca cgctggagct gctgggacgc gtgctccgcg acatggacct gctgggctgc 1620
ctggaggaca tcgaggaggc gctttgcggc cccgcgcgcc tcccgcgcgc gccagctctt 1680
ctcagatgag gctgcgcccc tgcgggcagc tctaaggacc gtcctgcgag atcgcttcc 1740
aacccactt ttttctggaa aggaggggtc ctgcaggggc aagcaggagc tagcagccgc 1800
ctacttggtg ctaacccctc gatgtacata gcttttctca gctgcctgcg cgccgccgac 1860
agtcagcgct gtgcgcgcgg agagaggtgc gccgtgggct caagagcctg agtgggtggt 1920
ttgcgaggat gagggacgct atgcctcatg cccgttttgg gtgtcctcac cagcaaggct 1980
gctcgggggc ccctggttcg tccctgagcc tttttcacag tgcataagca gttttttttg 2040
tttttgtttt gttttgtttt gtttttaaat caatcatggt acactaatag aaacttggca 2100
ctcctgtgcc ctctgcctgg acaagcacat agcaagctga actgtcctaa ggcagggggc 2160
agcacggaac aatggggcct tcagctggag ctgtggactt ttgtacatac actaaaattc 2220
tgaagttaaa gctctgctct tggagacagt ggct 2254

```

<210> 22

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 22

```

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
1      5      10      15
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20     25     30
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35     40     45
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50     55     60
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65     70     75     80
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85     90     95
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100    105    110
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
115    120    125

```

```

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
130 135 140
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145 150 155 160
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165 170 175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
180 185 190
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
195 200 205
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
210 215 220
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
225 230 235 240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
245 250 255
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
275 280 285
Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys
290 295 300
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
305 310 315 320
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
325 330 335
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
340 345 350
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
355 360 365
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
370 375 380
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
385 390 395 400
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
405 410 415
Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
420 425 430
Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
435 440 445
Pro Ala Pro Ser Leu Leu Arg
450 455

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<210> 23

<211> 2154

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 23

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cctctgactt tcagcttctc gaactcgagg cccaggctgc catcgcccg ggcacctggt 180
ccgatcatct tacttcattc acgagcggtt tcaattgctg ccctgtcccc agccccaatg 240
ggggagttag aggccactgc cggccggaca tgggtctccc caccgtgcct ggctgtctgc 300
tgtcactggt gtcctggct ctgctgatgg ggatacatcc atcaggggtc actggactag 360
tcccttctct tggtgaccgg gagaagaggg atagcttgtg tccccaagga aagtatgtcc 420

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attctaagaa caattccatc tgctgcacca agtgccacaa aggaacctac ttggtgagtg 480
actgtccgag cccaggggcg gatacagtct gcagggagtg tgaaaagggc acctttacgg 540
cttcccagaa ttacctcagg cagtgtctca gttgcaagac atgtcggaaa gaaatgtccc 600
aggtggagat ctctccttgc caagctgaca aggacacggt gtgtggctgt aaggagaacc 660
agttccaacg ctacctgagt gagacacact tccagtgcgt ggactgcagc cctgtcttca 720
acggcaccgt gacaatcccc tgtaaggaga ctgagaacac cgtgtgtaac tgccatgcag 780
ggttctttct gagagaaaagt gagtgcgtcc cttgcagcca ctgcaagaaa aatgaggagt 840
gtatgaagtt gtgcctacct cctccgcttg caaatgtcac aaacccccag gactcaggta 900
ctgcggtgct gttgcccctg gttatcttgc taggtctttg ccttctatcc tttatcttca 960
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ccttcagccc cacctccggc ttcaacccca ctctgggctt cagcacccca ggctttagtt 1140
ctcctgtctc cagtaccccc atcagcccca tcttcggctc tagtaactgg cacttcatgc 1200
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ctgacaatgc agaccttgcg attctgtatg ctgtggtgga tggcgtgcct ccagcgcgct 1380
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ctttttcact tttgataagc aatctttgta tcaattatat cacactaatg gatgaactgt 2040
gtaaggtaag gacaagcata gaaaggcggg gtctccagct ggagccctcg actcttgtaa 2100
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<210> 24

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 24

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Met Gly Leu Pro Thr Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu
 1          5          10          15
Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro
 20          25          30
Ser Leu Gly Asp Arg Glu Lys Arg Asp Ser Leu Cys Pro Gln Gly Lys
 35          40          45
Tyr Val His Ser Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50          55          60
Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Arg Asp Thr Val
 65          70          75          80
Cys Arg Glu Cys Glu Lys Gly Thr Phe Thr Ala Ser Gln Asn Tyr Leu
 85          90          95
Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Ser Gln Val
100          105          110
Glu Ile Ser Pro Cys Gln Ala Asp Lys Asp Thr Val Cys Gly Cys Lys
115          120          125
Glu Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys Val
130          135          140
Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu
145          150          155          160

```


Thr Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Arg Glu
 165 170 175
 Ser Glu Cys Val Pro Cys Ser His Cys Lys Lys Asn Glu Glu Cys Met
 180 185 190
 Lys Leu Cys Leu Pro Pro Pro Leu Ala Asn Val Thr Asn Pro Gln Asp
 195 200 205
 Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Leu Leu Gly Leu Cys
 210 215 220
 Leu Leu Ser Phe Ile Phe Ile Ser Leu Met Cys Arg Tyr Pro Arg Trp
 225 230 235 240
 Arg Pro Glu Val Tyr Ser Ile Ile Cys Arg Asp Pro Val Pro Val Lys
 245 250 255
 Glu Glu Lys Ala Gly Lys Pro Leu Thr Pro Ala Pro Ser Pro Ala Phe
 260 265 270
 Ser Pro Thr Ser Gly Phe Asn Pro Thr Leu Gly Phe Ser Thr Pro Gly
 275 280 285
 Phe Ser Ser Pro Val Ser Ser Thr Pro Ile Ser Pro Ile Phe Gly Pro
 290 295 300
 Ser Asn Trp His Phe Met Pro Pro Val Ser Glu Val Val Pro Thr Gln
 305 310 315 320
 Gly Ala Asp Pro Leu Leu Tyr Glu Ser Leu Cys Ser Val Pro Ala Pro
 325 330 335
 Thr Ser Val Gln Lys Trp Glu Asp Ser Ala His Pro Gln Arg Pro Asp
 340 345 350
 Asn Ala Asp Leu Ala Ile Leu Tyr Ala Val Val Asp Gly Val Pro Pro
 355 360 365
 Ala Arg Trp Lys Glu Phe Met Arg Phe Met Gly Leu Ser Glu His Glu
 370 375 380
 Ile Glu Arg Leu Glu Met Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
 385 390 395 400
 Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg His Glu Asp
 405 410 415
 Thr Leu Glu Val Val Gly Leu Val Leu Ser Lys Met Asn Leu Ala Gly
 420 425 430
 Cys Leu Glu Asn Ile Leu Glu Ala Leu Arg Asn Pro Ala Pro Ser Ser
 435 440 445
 Thr Thr Arg Leu Pro Arg
 450

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 25
 acagacaaac agcccaaacc

20

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 26
gcctcaccca tcagttgttt 20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 27
agatgtggat cagcaagcag 20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 28
gcgcaagtta ggttttgtca 20